

1 GCTGGATGGTGGACTCAGAGACCAATAAAAATAAACTGCTTGAACATCCTTTGACTGGTT  
 -----+-----+-----+-----+-----+-----+ 60  
 CGACCTACCACCTGAGTCTCIGGTTATTTTATTTGACGAACTTGTAGGAACTGACCAA  
  
 61 AGCCAGTTGCTGATGTATATICAAGATGAGTGGATTAGGAGAAAAGTTGGATCCACTGGC  
 -----+-----+-----+-----+-----+-----+ 120  
 TCGGTCAACGACTACATATAAGTTCTACTCACCTAATCCTCTTTTGAACCTAGGTGACCG  
  
 M S G L G E N L D P L A -  
  
 121 CAGTGATTACGAAAACGCAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAG  
 -----+-----+-----+-----+-----+-----+ 180  
 GTCACTAAGTGCTTTTGCCTTTAACGGTACACTATGAGGTCCTGTTCCAGAATGGACGTC  
  
 S D S R K R K L P C D T P G Q G L T C S -  
  
 181 TGGTGAAAAACGGAGACGGGAGCAGGAAAGTAAATATATTGAAGAATTGGCTGAGCTGAT  
 -----+-----+-----+-----+-----+-----+ 240  
 ACCACTTTTTGCCTCTGCCCTCGTCCCTTTCATTTATATAACTTCTTAACCGACTCGACTA  
  
 G E K R R R E Q E S K Y I E E L A E L I -  
  
 241 ATCTGCCAATCTTAGTGATAITGACAATTTCAATGTCAAACCAGATAAATGTGCGATTTT  
 -----+-----+-----+-----+-----+-----+ 300  
 TAGACGGTTAGAATCACTATAACTGTAAAGTTACAGTTTGGTCTATTTACACGCTAAAA  
  
 S A N L S D I D N F N V K P D K C A I L -  
  
 301 AAAGGAAACAGTAAGACAGATACGTCAAATAAAAGAGCAAGGAAAAAGTATTTCCAATGA  
 -----+-----+-----+-----+-----+-----+ 360  
 TTTCTTTTGTCAATCTGTCTATGCAGTTTATTTTCTCGTTCCTTTTGTATAAAGGTTACT  
  
 K E T V R Q I R Q I K E Q G K T I S N D -  
  
 361 TGATGATGTTCAAAAAGCCGATGTATCTTCTACAGGGCAGGGAGTTATTGATAAAGACTC  
 -----+-----+-----+-----+-----+-----+ 420  
 ACTACTACAAGTTTTTCGGCTACATAGAAGATGTCCCGTCCCTCAATAACTATTTCTGAG  
  
 D D V Q K A D V S S T G Q G V I D K D S -  
  
 421 CTTAGGACCGCTTTTACTTCAGGCATTGGATGGTTTCTTATTTGTGGTGAATCGAGAGGC  
 -----+-----+-----+-----+-----+-----+ 480  
 GAATCCTGGCGAAAATGAAGTCCGTAACCTACCAAAGGATAAACACCACTTAGCTCTCCG  
  
 L G P L L L Q A L D G F L F V V N R E A -  
  
 481 AAACATTGTATTTGTATCAGAAAATGTCACACAATACCTGCAATATAAGCAAGAGGACCT  
 -----+-----+-----+-----+-----+-----+ 540  
 TTTGTAACATAAACATAGTCTTTTACAGTGTGTTATGGACGTTATATTCGTTCTCTTGA  
  
 N I V F V S E N V T Q Y L Q Y K Q E D L -  
  
 541 GGTAAACACAAGTGTTTACAATATCTTACATGAAGAAGACAGAAAGGATTTTCTTAAGAA  
 -----+-----+-----+-----+-----+-----+ 600  
 CCAATTGTGTTCACAAATGTATAGAATGTACTTCTTCTGTCTTTCCTAAAAGAATTCTT

FIGURE 1

V N T S V Y N I L H E E D R K D F L K N -  
 TTTACCAAATCTACAGTTAATGGAGTTTCCTGGACAAATGAGACCCAAAGACAAAAAG  
 601 -----+-----+-----+-----+-----+ 660  
 AAATGGTTTTAGATGTCAATTACCTCAAAGGACCTGTTTACTCTGGGTTTCTGTTTTTC  
 L P K S T V N G V S W T N E T Q R Q K S -  
 TCATACATTTAATTGCCGTATGTTGATGAAAACACCACATGATATTCTGGAAGACATAAA  
 661 -----+-----+-----+-----+-----+ 720  
 GGTATGTAAATTAACGGCATACAACTACTTTTGTGGTGTACTATAAGACCTTCTGTATTT  
 H T F N C R M L M K T P H D I L E D I N -  
 CGCCAGTCCTGAAATGCGCCAGAGATATGAAACAATGCAGTGCTTTGCCCTGTCTCAGCC  
 721 -----+-----+-----+-----+-----+ 780  
 GCGGTCAGGACTTTACGCGGTCTCTATACTTTGTTACGTCACGAAACGGGACAGAGTCGG  
 A S P E M R Q R Y E T M Q C F A L S Q P -  
 ACGAGCTATGATGGAGGAAGCGGAAGATTTGCAATCTTGTATGATCTGTGTGGCAGCCG  
 781 -----+-----+-----+-----+-----+ 840  
 TGCTCGATACTACCTCCTTCCCTTCTAAACGTTAGAACATACTAGACACACCGTGCGGC  
 R A M M E E G E D L Q S C M I C V A R R -  
 CATTACTACAGGAGAAAGAACATTTCCATCAAACCCTGAGAGCTTTATTACCAGACATGA  
 841 -----+-----+-----+-----+-----+ 900  
 GTAATGATGTCCTCTTTCTTGTAAGGTAGTTTGGGACTCTCGAAATAATGGTCTGTACT  
 I T T G E R T F P S N P E S F I T R H D -  
 TCTTTCAGGAAAGGTTGTCAATATAGATACAAATTCAGTACTGAGATCCTCCATGAGGCCTGG  
 901 -----+-----+-----+-----+-----+ 960  
 AGAAAGTCCTTTCCAACAGTTATATCTATGTTTAAGTGACTCTAGGAGGTACTCCGGACC  
 L S G K V V N I D T N S L R S S M R P G -  
 CTTTGAAGATATAATCCGAAGGTGTATTCAGAGATTTTTTTAGTCTAAATGATGGGCAGTC  
 961 -----+-----+-----+-----+-----+ 1020  
 GAAACTTCTATATTAGGCTTCCACATAAGTCTCTAAAAAATCAGATTTACTACCCGTCAG  
 F E D I I R R C I Q R F F S L N D G Q S -  
 ATGGTCCCAGAAACGTCAGTATCAAGAAGCTTATCTTAATGGCCATGCAGAAACCCAGT  
 1021 -----+-----+-----+-----+-----+ 1080  
 TACCAGGGTCTTTGCAGTGATAGTTCTTCGAATAGAATTACCGGTACGTCTTTGGGGTCA  
 W S Q K R H Y Q E A Y L N G H A E T P V -  
 ATATCGATTCTCGTTGGCTGATGGAAGTATAGTGACTGCACAGACAAAAAGCAAACCTTT  
 1081 -----+-----+-----+-----+-----+ 1140  
 TATAGCTAAGAGCAACCGACTACCTTGATATCACTGACGTGTCTGTTTTTCGTTTGAGAA  
 Y R F S L A D G T I V T A Q T K S K L F -  
 CCGAAATCCTGTAACAAATGATCGACATGGCTTTGTCTCAACCCACTTCCTTCAGAGAGA  
 1141 -----+-----+-----+-----+-----+ 1200  
 GGCTTTAGGACATTGTTTACTAGCTGTACCGAAACAGAGTTGGGTGAAGGAAGTCTCTCT  
 R N P V T N D R H G F V S T H F L Q R E -

FIGURE 1A

ACAGAATGGATATAGACCAAPCCCAAATCCTGTTGGACAAGGGATTAGACCACCTATGGC  
 1201 -----+-----+-----+-----+-----+-----+ 1260  
 TGTCTTACCTATATCTGGTTIGGGTTTAGGACAACCTGTTCCCTAATCTGGTGGATACCG  
 Q N G Y R P N P N P V G Q G I R P P M A -  
 TGGATGCAACAGTTTCGGTAGGCGGCATGAGTATGTGCGCAAACCAAGGCTTACAGATGCC  
 1261 -----+-----+-----+-----+-----+-----+ 1320  
 ACCTACGTTGTCAAGCCATCCGCCGTACTCATAACAGCGGTTTGGTTCCGAATGTCTACGG  
 G C N S S V G G M S M S P N Q G L Q M P -  
 GAGCAGCAGGGCCTATGGCTTGGCAGACCCTAGCACCACAGGGCAGATGAGTGGAGCTAG  
 1321 -----+-----+-----+-----+-----+-----+ 1380  
 CTCGTCGTCCCGGATACCGAACCGTCTGGGATCGTGGTGTCCCGTCTACTCACCTCGATC  
 S S R A Y G L A D P S T T G Q M S G A R -  
 GTATGGGGGTTCCAGTAACAAGCTTCATTGACCCCTGGGGCCAGGCATGCAATCACCATC  
 1381 -----+-----+-----+-----+-----+-----+ 1440  
 CATACCCCCAAGGTCATTGTATCGAAGTAAGTGGGGACCCGGTCCGTACGTTAGTGGTAG  
 Y G G S S N I A S L T P G P G M Q S P S -  
 TTCCTACCAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCACATGGGAGTCCTGG  
 1441 -----+-----+-----+-----+-----+-----+ 1500  
 AAGGATGGTCTTGTGTTGATACCCGAGTTGTACTCATCGGGGGGTGTACCCTCAGGACC  
 S Y Q N N N Y G L N M S S P P H G S P G -  
 TCTTGCCCCAAACCAGCAGAAATATCATGATTTCTCCTCGTAATCGTGGGAGTCCAAAGAT  
 1501 -----+-----+-----+-----+-----+-----+ 1560  
 AGAACGGGGTTTGGTCGTCTIATAGTACTAAAGAGGAGCATTAGCACCCCTCAGGTTTCTA  
 L A P N Q Q N I M I S P R N R G S P K I -  
 AGCCTCACATCAGTTTTTCTCCTGTTGCAGGTGTGCACTCTCCCATGGCATCTTCTGGCAA  
 1561 -----+-----+-----+-----+-----+-----+ 1620  
 TCGGAGTGTAGTCAAAAGAGGACAACGTCCACACGTGAGAGGGTACCGTAGAAGACCGTT  
 A S H Q F S P V A G V H S P M A S S G N -  
 TACTGGGAACCACAGCTTTTTCAGCAGCTCTCTCAGTGCCCTGCAAGCCATCAGTGAAGG  
 1621 -----+-----+-----+-----+-----+-----+ 1680  
 ATGACCCTTGGTGTGCAAAAGGTCGTGAGAGAGTCACGGGACGTTCCGGTAGTCACTTCC  
 T G N H S F S S S S L S A L Q A I S E G -  
 TGTGGGGACTTCCCTTTTATCTACTCTGTATCACCAGGCCCCAAATTGGATAACTCTCC  
 1681 -----+-----+-----+-----+-----+-----+ 1740  
 ACACCCCTGAAGGGAAAATAGATGAGACAGTAGTGGTCCGGGGTTTAACCTATTGAGAGG  
 V G T S L L S T L S S P G P K L D N S P -  
 CAATATGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTCCAAGAGTCCTCTGGG  
 1741 -----+-----+-----+-----+-----+-----+ 1800  
 GTTATACTTATAATGGGTTGCTTCATTTTCATTCGTTAGTCCTAAGGTTCTCAGGAGACCC  
 N M N I T Q P S K V S N Q D S K S P L G -  
 CTTTTATTGCGACCAAAATCCAGTGGAGAGTTCAATGTGTCTAGTCAAATAGCAGAGATCA

FIGURE 1B

1801 -----+-----+-----+-----+-----+-----+-----+ 1860  
 GAAAATAACGCTGGTTTTAGGTCACCTCTCAAGTTACACAGTCAGTTTATCGTCTCTAGT  
 F Y C D Q N P V E S S M C Q S N S R D H -  
 -CTCAGTGACAAAGAAAGTAAAGGAGAGCAGTGTTGAGGGGGCAGAGAATCAAAGGGGTCC  
 1861 -----+-----+-----+-----+-----+-----+-----+ 1920  
 GGAGTCACTGTTTCTTTTCATTCTCTCGTCACAACCTCCCCCGTCTCTTAGTTTCCCCCAGG  
 L S D K E S K E S S V E G A E N Q R G P -  
 TTTGGAAAGCAAAGGTCATAA AAAATTACTGCAGTTACTTACCTGTTCTTCTGATGACCG  
 1921 -----+-----+-----+-----+-----+-----+-----+ 1980  
 AAACCTTTTCGTTTCCAGTATTTTAAATGACGTCAATGAATGGACAAGAAGACTACTGGC  
 L E S K G H K K L L Q L L T C S S D D R -  
 GGGTCATTCCCTCCTTGACCAACTCCCCCCTAGATTCAAGTTGTAAAGAATCTTCTGTTAG  
 1981 -----+-----+-----+-----+-----+-----+-----+ 2040  
 CCCAGTAAGGAGGAAGTGGTGGAGGGGGATCTAAGTTCAACATTTCTTAGAAGACAATC  
 G H S S L T N S P L D S S C K E S S V S -  
 TGTCACCAGCCCCCTCTGGAGTCTCCTCCTCTACATCTGGAGGAGTATCCTCTACATCCAA  
 2041 -----+-----+-----+-----+-----+-----+-----+ 2100  
 ACAGTGGTTCGGGGAGACCTCAGAGGAGGAGATGTAGACCTCCTCATAGGAGATGTAGGTT  
 V T S P S G V S S S T S G G V S S T S N -  
 TATGCATGGGTCACTGTTACAAGAGAAGCACCGGATTTTGCACAAGTTGCTGCAGAATGG  
 2101 -----+-----+-----+-----+-----+-----+-----+ 2160  
 ATACGTACCCAGTGACAATGTCTCTTCGTGGCCTAAACGTGTTCAACGACGTCTTACC  
 M H G S L L Q E K H R I L H K L L Q N G -  
 GAATTCACCAGCTGAGGTAGCCAAGATTACTGCAGAAGCCACTGGGAAAGACACCAGCAG  
 2161 -----+-----+-----+-----+-----+-----+-----+ 2220  
 CTTAAGTGGTCGACTCCATCGGTTCTAATGACGTCTTCGGTGACCCTTTCTGTGGTTCGTC  
 N S P A E V A K I T A E A T G K D T S S -  
 TATAACTTCTTGTGGGGACGCAATGTTGTCAAGCAGGAGCAGCTAAGTCCTAAGAAGAA  
 2221 -----+-----+-----+-----+-----+-----+-----+ 2280  
 ATATTGAAGAACACCCCTGCCTTTACAACAGTTCGTCCTCGTCGATTCAGGATTCTTCTT  
 I T S C G D G N V V K Q E Q L S P K K K -  
 GGAGAATAATGCACCTTCTTAGATACCTGCTGGACAGGGATGATCCTAGTGATGCACCTCTC  
 2281 -----+-----+-----+-----+-----+-----+-----+ 2340  
 CCTCTTATTACGTGAAGAATCTATGGACGACCTGTCCCTACTAGGATCACTACGTGAGAG  
 E N N A L L R Y L L D R D D P S D A L S -  
 TAAAGAACTACAGCCCCAAGTGAAGGAGTGGACAATAAAATGAGTCAGTGCACCAGCTC  
 2341 -----+-----+-----+-----+-----+-----+-----+ 2400  
 ATTTCTTGATGTCGGGGTTCACCTTCCTCACCTGTTATTTTACTCAGTCACGTGGTCT 37.3  
 K E L Q P Q V E G V D N K M S Q C T S S -  
 CACCATTCCCTAGCTCAAGTCAAGAGAAAGACCCTAAAATTAAGACAGAGACAAGTGAAGA  
 2401 -----+-----+-----+-----+-----+-----+-----+ 2460  
 GTGGTAAGGATCGAGTTCAGTCTCTTTCTGGGATTTTAATTCTGTCTCTGTTCACTTCT

FIGURE 1C

T I P S S S Q E K D P K I K T E T S E E -  
 2461 GGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTGACTT  
 -----+-----+-----+-----+-----+ 2520  
 CCCTAGACCTCTGAACCTATTAGATCTACGATAAGAACCCTAGACTGATCAAGACTGAA  
 G S G D L D N L D A I L G D L T S S D F -  
 2521 TTACAATAATTCCATATCCTCAAATGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCA  
 -----+-----+-----+-----+-----+ 2580  
 AATGTTATTAAGGTATAGGAGTTTACCATCAGTAGACCCCTGATTTCGTTGTCCACAAAGT  
 Y N N S I S S N G S H L G T K Q Q V F Q -  
 2581 AGGAACTAATTCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTTCGTCTCCATA  
 -----+-----+-----+-----+-----+ 2640  
 TCCTTGATTAAAGAGACCCAACTTTTCAAGTGTGACACGTCAGATAAGCAGGAGGTAT  
 G T N S L G L K S S Q S V Q S I R P P Y -  
 2641 TAACCGAGCAGTGTCTCTGGATAGCCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAAA  
 -----+-----+-----+-----+-----+ 2700  
 ATTGGCTCGTCAAGAGACCTATCGGGACAAAGACAACCGAGTTCAGGAGGTCATTTTTT  
 N R A V S L D S P V S V G S S P P V K N -  
 2701 ATCAGTGCTTTCCCATGTACCAAAGCAACCCATGTTGGGTGGGAATCCAAGAATGAT  
 -----+-----+-----+-----+-----+ 2760  
 ATAGTCACGAAAGGGGTACAATGGTTTCGTTGGGTACAACCCACCCTTAGGTTCTTACTA  
 I S A F P M L P K Q P M L G G N P R M M -  
 2761 GGATAGTCAGGAAAATTATGGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTGTGAC  
 -----+-----+-----+-----+-----+ 2820  
 CCTATCAGTCCTTTTAATACCGAGTTCATACCCACCCGGTTTGGCTTTACACTGACACTG  
 D S Q E N Y G S S M G G P N R N V T V T -  
 2821 TCAGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACCTCAAAGGCCGGCAGAATGGAACC  
 -----+-----+-----+-----+-----+ 2880  
 AGTCTGAGGAAGGAGTCCTCTGACCCCGAATGGTTTGAGTTTCCGGCCGTCTTACCTTGG  
 Q T P S S G D W G L P N S K A G R M E P -  
 2881 TATGAATTCAAACCTCCATGGGAAGACCAGGAGGAGATTATAATACTTCTTTACCCAGACC  
 -----+-----+-----+-----+-----+ 2940  
 ATACTTAAGTTTGAGGTACCCCTTCTGGTCTCTCTAATATTATGAAGAAATGGGTCTGG  
 M N S N S M G R P G G D Y N T S L P R P -  
 2941 TGCACTGGGTGGCTCTATTCCACATTGCCTCTTCGGTCTAATAGCATACCCAGGTGCGAG  
 -----+-----+-----+-----+-----+ 3000  
 ACGTGACCCACCGAGATAAGGGTGTAACGGAGAAGCCAGATTATCGTATGGTCCACGCTC  
 A L G G S I P T L P L R S N S I P G A R -  
 3001 ACCAGTATTGCAACAGCAGCAGCAGATGCTTCAAATGAGGCCTGGTGAAATCCCCATGGG  
 -----+-----+-----+-----+-----+ 3060  
 TGGTCATAACGTTGTCGTCGTCGTCTACGAAGTTTACTCCGGACCACTTTAGGGGTACCC  
 P V L Q Q Q Q Q M L Q M R P G E I P M G -

FIGURE 1D



[illegible]

FIGURE 1F

G H M G Q M N M N P M P M S G M P M G P -

4321 TGATCAGAAATACTGCTGACATCTCTGCACCAGGACCTCTTAAGGAAACCACTGTACAAA  
-----+-----+-----+-----+-----+ 4380  
ACTAGTCTTTATGACGACTGAGAGACGTGGTCCTGGAGAATTCCTTTGGTGACATGTTT

D Q K Y C \*

4381 TGACACTGCACTAGGATTATIGGGAAGGAATCATTGTTCCAGGCATCCATCTTGGAAGAA  
-----+-----+-----+-----+-----+ 4440  
ACTGTGACGTGATCCTAATAACCCCTTCCTTAGTAACAAGGTCCGTAGGTAGAACCTTCTT

4441 AGGACCAGCTTTGAGCTCCATCAAGGGTATTTTAAGTGATGTCATTTGAGCAGGA  
-----+-----+-----+-----+-----+ 4495  
TCCTGGTCGAAACTCGAGGTAGTTCCTCCATAAAATTCCTACAGTAAACTCGTCCT

004194-0393  
06EFD-1667060



1 MSGLGENLDP LASDS <sup>bHLH domain</sup> PKRKL PCDTPGQGLT CSGEKRRREQ ESKYIEELAE  
 51 LISANLS DID NFNVKPDKCA ILKETVRQIR QIKE QGKTIS NDDDVQKADV  
 101 SSTGQGVIDK DSLGPLLLQA <sup>PAS 'A' domain</sup> LDGFLFVVNR EANIVFVSEN VTOYLOYKOE  
 151 DLVNTSVYNI LHEEDRKDFL KNLPKSTVNG VSWTNEPQRQ KSHTFNCRML  
 201 MKTPHDILED INASPEMRQR YETMQCFALS QPRAMMEEGE DLQSCMICVA  
 251 RRITTGERTF PSNPES <sup>PAS 'B' domain</sup> FITR HDLSGKV VNI DTNSLRSSMR PGFEDIIRRC  
 301 IQRFFSLNDG QWSQKRHYQ EAYLNGHA ET PVYRFS LADG TIVTAQTKSK  
 351 LFRNPVTNDR HGFVSTHFLQ REQNGYRPNP NPVGQGIRPP MAGCNSSVGG  
 401 <sup>→ RAC3.1</sup> MSMSPNQGLQ MPSSRAYGLA DPSTTGQMSG ARYGGSSNIA SLTPGPGMQS  
 451 PSSYQNNNYG LNMSSPPHGS PGLAPNQONI MISPRNRGSP KIASHQFSPV  
 501 AGVHSPMASS GNTGNHSFSS SLSALQAIS EGVGTSLLST LSSPGPKLDN  
 551 SPNMNITQPS KVSNQDSKSP LGFYCDQNPV ESSMCQNSR DHLSDKESKE  
 601 SSVEGAENQR GPLESKGHKK <sup>i</sup> LLQLLTCSSD DRGHSSLTNS PLDSSCKESS  
 651 VSVTSPSGVS SSTSGGVSST SNMHGSL LQE <sup>ii</sup> KHRLLHKLLO NGNSPAEVAK  
 701 ITAEATGKDT SSITSCGDGN VVKQEQLSPK <sup>iii</sup> KKENNAL LRY LLDRDDPSDA  
 751 LSKELQPQVE GVDNKMSQCT SSTIPSSSQE KDPKIKTETS EEGSGDL DNL  
 801 <sup>iv</sup> DAILLGDLTSS DFYNNSISSN GSHLGTKQV FQGTNSLGLK SSQSVQSIRP  
 851 PYNRAVSLDS PVSVGSSPPV KNISAFPMLP KQFMLGGNPR MMDSQENYGS  
 901 SMGGPNRNV TQTTPSSGDW GLPNSKAGRM EPMNSNSMGR PGGDYNTSLP  
 951 RPALGGS IPT LPLRSNSIPG ARPVLQQQQQ MLQMRPGEIP MGMGANPYGQ  
 1001 AAASNQLGSW PDGMLSMEQV SHGTQNRPLL RNSLDDL VGP PSNLEGQSDE  
 1051 <sup>v</sup> RALLDQLHTL LSNTDATGLE <sup>vi</sup> EIDRALG IPE LVNQQALEP KQDAFQGQEA  
 1101 AVMMDQKAGL YGQTYPAQGP PMQGGFHLQG QSPSFNSMMN QMNQQGNFPL  
 1151 QGMHPRANIM <sup>Q-rich domain</sup> RPRNTNPKQL RMQLQORLOG QQFLNQSRQA LELKMNPTA  
 1201 <sup>← RAC3.1</sup> GGAAVMRPMM QPQOGFLNAQ MVAQRSRELL SHHFROORVA MMMQQQQQQQ  
 1251 QQQQQQQQQQ QQQQQQQQQT QAFSPPPNVT ASPSMGLLA GPTMPQAPPQ  
 1301 QFPYQPNYGM GQQPDPAFGR VSSPPNAMMS SRMGPSQNPM MQHPQAASIY  
 1351 QSSEMKGWPS GNLA RNSSFS QQQFAHQGNP AVYSMVHMNG SSGHMGQMNM  
 1401 NPM PMSGMPM GPDQKYC\*

FIGURE 2



8667E0 465TH060

i.	SKGHKKLLQLLTCSSDD	RAC3	(615-631)
	SKGQTKLLQLLTTKSDD	TIF2	(840-651)
	SQTSHKLVOLLTTTAAE	SRC1	(632-643)
ii.	LQEKHRLHKKLLQNGNSP	RAC3	(678-695)
	LKEKHKILHRLQLDSSSP	TIF2	(683-699)
	LTERHKILHRLQEG.SP	SRC1	(683-699)
iii.	KKKE...NNALLRYLLDRDDPSD	RAC3	(730-749)
	KKKE...NNALLRYLLDKDDTKD	TIF2	(738-753)
	KKKESKDHQLLRYLLDKDE.KD	SRC1	(739-757)
iv.	DLDNLDAILGDL	RAC3	(796-807)
	ELDNLEEILDDL	TIF2	(803-814)
	DLQFDQLLPTL	SRC1	(810-821)
v.	EGQSDERALLDQLHTLL	RAC3	(1045-1061)
	ESPSDEGALLDQLYLAL	TIF2	(1071-1087)
	EGRNDEKALLEQLVSFL	SRC1	(924-940)
vi.	LEEIDRALGIPELVNQ	RAC3	(1069-1084)
	LEEIDRALGIPELVSO	TIF2	(1093-1108)
	LAELDRALGIDKLV.Q	SRC1	(948-962)
vii.	QTPQAQKSLLQQLUTE*	SRC1	(1424-1440)

FIGURE 4

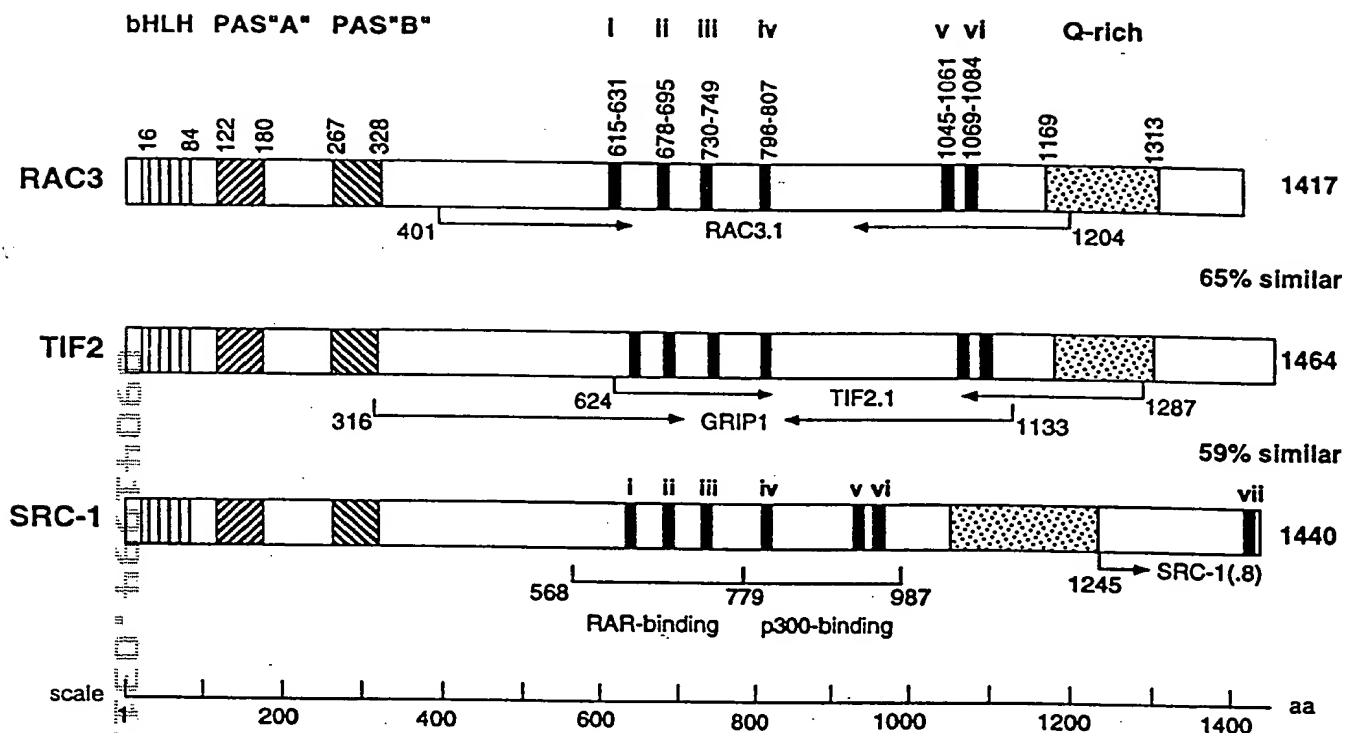


FIGURE 5

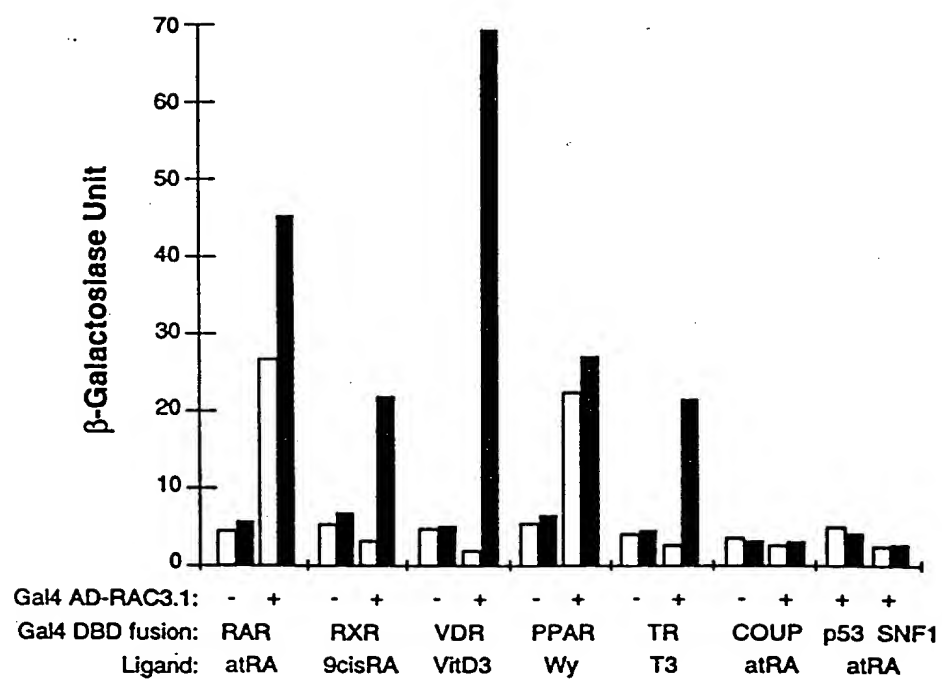


FIGURE 6

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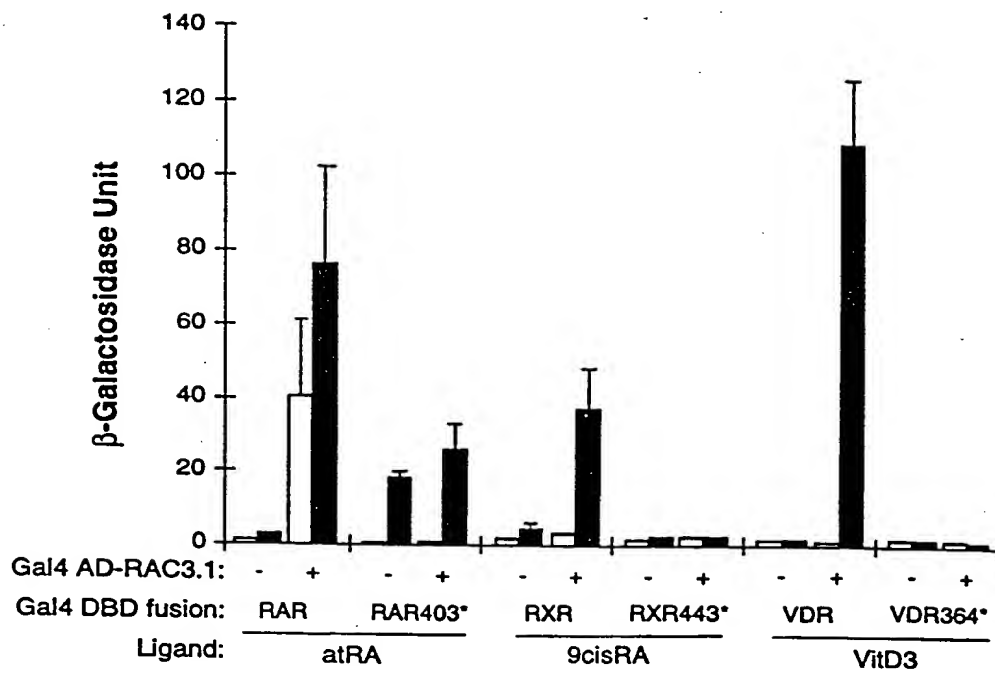


FIGURE 7

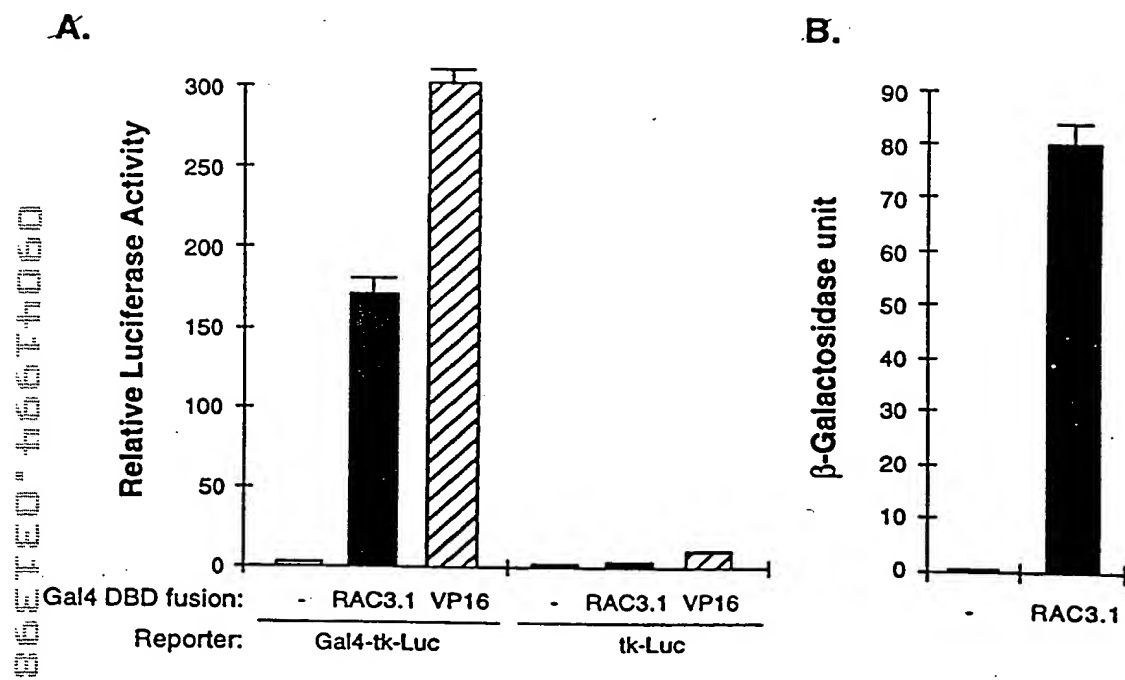


FIGURE 8

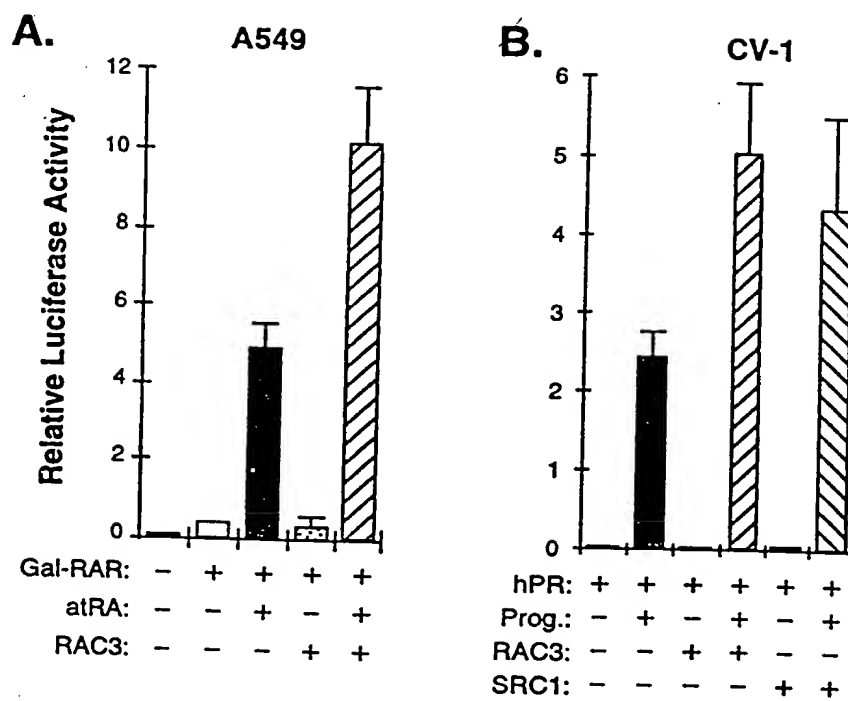


FIGURE 9